

ID AC020568 standard; DNA; HTG; 192618 BP.

XX

AC AC020568;

XX

SV AC020568.4

XP-002192687

XX

DT 06-JAN-2000 (Rel. 62, Created)

DT 21-JUL-2000 (Rel. 64, Last updated, Version 4)

XX

DE Homo sapiens chromosome 20 clone RP11-206C1, WORKING DRAFT SEQUENCE, 24
DE unordered pieces.

XX

KW HTG; HTGS_DRAFT; HTGS_PHASE1.

XX

OS Homo sapiens (human)

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;

OC Eutheria; Primates; Catarrhini; Hominidae; Homo.

XX

RN [1]

RP 1-192618

RA Waterston R.H.;

RT "The sequence of Homo sapiens clone";

RL Unpublished.

XX

RN [2]

RP 1-192618

RA Waterston R.H.;

RT ;

RL Submitted (04-JAN-2000) to the EMBL/GenBank/DDBJ databases.

RL Genome Sequencing Center, Washington University School of Medicine, 4444
RL Forest Park Parkway, St. Louis, MO 63108, USA

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CC On Jul 19, 2000 this sequence version replaced gi:9211362.

CC ----- Genome Center -----

CC Center: Washington University Genome Sequencing Center

CC Center code: WUGSC

CC Web site:<http://genome.wustl.edu/gsc/index.shtml>

CC ----- Project Information -----

CC Center project name: H_NH0206C01

CC ----- Summary Statistics -----

CC Sequencing vector: M13; 93%

CC Sequencing vector: plasmid; 7%

CC Chemistry: Dye-primer ET; 93% of reads

CC Chemistry: Dye-terminator Big Dye; 7% of reads

CC Assembly program: Phrap; version 0.990319

CC Consensus quality: 179082 bases at least Q40

CC Consensus quality: 183120 bases at least Q30

CC Consensus quality: 185448 bases at least Q20

CC Insert size: 205000; agarose-fp

CC Insert size: 190318; sum-of-contigs

CC Quality coverage: 3.99 in Q20 bases; agarose-fp

CC Quality coverage: 4.34 in Q20 bases; sum-of-contigs

CC -----

CC * NOTE: This is a 'working draft' sequence. It currently

CC * consists of 24 contigs. The true order of the pieces

CC * is not known and their order in this sequence record is

CC * arbitrary. Gaps between the contigs are represented as

CC * runs of N, but the exact sizes of the gaps are unknown.

CC * This record will be updated with the finished sequence

CC * as soon as it is available and the accession number will

CC * be preserved.

CC * 1 1279: contig of 1279 bp in length

CC * 1280 1379: gap of unknown length

CC * 1380 3544: contig of 2165 bp in length

CC * 3545 3644: gap of unknown length

CC * 3645 5441: contig of 1797 bp in length

CC * 5442 5541: gap of unknown length

CC * 5542 8421: contig of 2880 bp in length

CC * 8422 8521: gap of unknown length

CC * 8522 10096: contig of 1575 bp in length

CC * 10097 10196: gap of unknown length

CC * 10197 11938: contig of 1742 bp in length

P.D. 06-01-2009

p. 1-5 = 5

CC * 11939 12038: gap of unknown length
 CC * 12039 14708: contig of 2670 bp in length
 CC * 14709 14808: gap of unknown length
 CC * 14809 17876: contig of 3068 bp in length
 CC * 17877 17976: gap of unknown length
 CC * 17977 21534: contig of 3558 bp in length
 CC * 21535 21634: gap of unknown length
 CC * 21635 24615: contig of 2981 bp in length
 CC * 24616 24715: gap of unknown length
 CC * 24716 28301: contig of 3586 bp in length
 CC * 28302 28401: gap of unknown length
 CC * 28402 35969: contig of 7568 bp in length
 CC * 35970 36069: gap of unknown length
 CC * 36070 42473: contig of 6404 bp in length
 CC * 42474 42573: gap of unknown length
 CC * 42574 49752: contig of 7179 bp in length
 CC * 49753 49852: gap of unknown length
 CC * 49853 57604: contig of 7752 bp in length
 CC * 57605 57704: gap of unknown length
 CC * 57705 67088: contig of 9384 bp in length
 CC * 67089 67188: gap of unknown length
 CC * 67189 77656: contig of 10468 bp in length
 CC * 77657 77756: gap of unknown length
 CC * 77757 92143: contig of 14387 bp in length
 CC * 92144 92243: gap of unknown length
 CC * 92244 109240: contig of 16997 bp in length
 CC * 109241 109340: gap of unknown length
 CC * 109341 124285: contig of 14945 bp in length
 CC * 124286 124385: gap of unknown length
 CC * 124386 138608: contig of 14223 bp in length
 CC * 138609 138708: gap of unknown length
 CC * 138709 153882: contig of 15174 bp in length
 CC * 153883 153982: gap of unknown length
 CC * 153983 169994: contig of 16012 bp in length
 CC * 169995 170094: gap of unknown length
 CC * 170095 192618: contig of 22524 bp in length.
 XX

FH	Key	Location/Qualifiers
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FT	misc_feature	1..1279 /note="assembly_name:Contig19"
FT	misc_feature	1380..3544 /note="assembly_name:Contig21"
FT	misc_feature	3645..5441 /note="assembly_name:Contig22"
FT	misc_feature	5542..8421 /note="assembly_name:Contig23"
FT	misc_feature	8522..10096 /note="assembly_name:Contig24"
FT	misc_feature	10197..11938 /note="assembly_name:Contig25"
FT	misc_feature	12039..14708 /note="assembly_name:Contig26"
FT	misc_feature	14809..17876 /note="assembly_name:Contig27"
FT	misc_feature	17977..21534 /note="assembly_name:Contig28"
FT	misc_feature	21635..24615 /note="assembly_name:Contig29"
FT	misc_feature	24716..28301 /note="assembly_name:Contig30"
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FT	misc_feature	153983..169994	
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FT	misc_feature	/note="assembly_name:Contig43"	
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